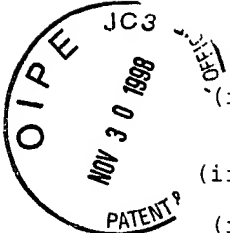


SEQUENCE LISTING

#8/C

(1) GENERAL INFORMATION:

- (i) APPLICANT: KAYAGAKI, Nobuhiko
YAGITA, Kideo
OKUMURA, Ko
NAKATA, Motomi
- (ii) TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF
- (iii) NUMBER OF SEQUENCES: 31
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: McDermott, Will & Emery
(B) STREET: 99 Canal Center Plaza, Suite 300
(C) CITY: Alexandria
(D) STATE: Virginia
(E) COUNTRY: USA
(F) ZIP: 22314
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/913,555
(B) FILING DATE: 19-SEP-1997
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Bucca Ph.D., Daniel
(B) REGISTRATION NUMBER: 42,368
(C) REFERENCE/DOCKET NUMBER: 50356-150
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202-756-8600
(B) TELEFAX: 202-756-8699



(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gln | Leu | Gln | Glu | Ser | Gly | Pro | Glu | Leu | Val | Lys | Pro | Gly | Ala | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Lys | Ile | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Ala | Phe | Ser | Ser | Trp | |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Met | Asn | Trp | Val | Lys | Gln | Arg | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Ile | Gly |
| | | 35 | | | | | 40 | | | | | 45 | | | |

Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Asp Asn Gly Lys Phe Lys
 50 55 60
 Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met
 65 70 75 80
 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
 85 90 95
 Arg Ser Tyr Tyr Tyr Asp Gly Ser Pro Trp Phe Thr Tyr Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGCAGCTGC AGGAGTCTGG ACCTGAGCTG GTGAAGCCTG GGCCTCAGT GAAGATTTCC	60
TGCAAGGCTT CTGGCTATGC ATTCAGTAGC TCCTGGATGA ACTGGGTGAA GCAGAGGCCT	120
GGAAAGGGTC TTGAGTGGAT TGGACGAATT TATCCTGGAG ATGGAGATAC TAACGACAAC	180
GGGAAGTTCA AGGGCAAGGC CAACTGACC GCAGACAAAT CCTCCAGCAC AGCCTACATG	240
CAACTCAGCA GTCTGACATC TGAGGACTCT GCGGTCTACT TCTGTGCAAG ATCGTATTAC	300
TACGATGGTA GCCCCTGGTT TACTTACTGG GGCCAAGGGA CCACGGTCAC CGTCTCCTCA	360

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15
 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 35 40 45

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Ser Glu Phe Pro Trp
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GACATCCAGA TGACGCAGTC TCCATCCTCC CTGTCTGCCT CTCTGGGAGA CAGAGTCACC	60
ATCAGTTGCA GGGCAAGTCA GGATATTAGC AATTATTTAA ACTGGTATCA GCAGAAACCA	120
GATGGAAGTCT TAAACTCCT GATCTACTAC ACATCAAGAT TAACTCAGG AGTCCCATCA	180
AGGTTCAAGTGC GAGTGGGTC TGGGACAGAT TATTCTCTCA CCATCAGCAA CCTGGAACCT	240
GAAGATATTG CCACTTACTT TTGTCAGCAA TATAGTGAAT TTCCGTGGAC GTTCGGTGA	300
GGCACCAAGC TGGAAATCAA ACGG	324

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Thr Ser
 1 5 10 15
 Val Lys Met Ser Cys Lys Ala Ala Gly Tyr Thr Phe Thr Asn Tyr Trp
 20 25 30
 Ile Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly
 35 40 45
 Tyr Leu Tyr Pro Gly Gly Leu Tyr Thr Asn Tyr Asn Glu Lys Phe Lys
 50 55 60
 Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr Met

65		70		75		80									
Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Ile	Tyr	Tyr	Cys	Ala
			85						90					95	
Arg	Tyr	Arg	Asp	Tyr	Asp	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
			100					105					110		
Thr	Val	Thr	Val	Ser	Ser										
			115												

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGCAGCTGC AGCAGTCAGG AGCTGAGCTG GTAAGGCCTG GGACTTCAGT GAAGATGTCC	60
TGCAAGGCTG CTGGATACAC CTTCACTAAC TACTGGATAG GTTGGGTAAA GCAGAGGCCT	120
GGACATGGCC TTGAGTGGAT TGGATATCTT TACCCTGGAG GTCTTTATAC TAACTACAAT	180
GAGAAGTTCA AGGGCAAGGC CACACTGACT GCAGACACAT CCTCCAGCAC AGCCTACATG	240
CAGCTCAGCA GCCTGACATC TGAGGACTCT GCCATCTATT ACTGTGCAAG ATACAGGGAT	300
TACGACTATG CTATGGACTA CTGGGGCCAA GGGACCACGG TCACCGTCTC CTCA	354

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp	Val	Leu	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Asn	Ile	Gly
1				5				10					15		
Asp	Gln	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Thr	Lys	Ser	Leu	Leu	Asn	Ser
		20					25					30			
Asp	Gly	Phe	Thr	Tyr	Leu	Gly	Trp	Cys	Leu	Gln	Lys	Pro	Gly	Gln	Ser
		35				40					45				
Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro
	50					55				60					
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65					70				75					80	

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Ser
85 90 95

Asn Tyr Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GATGTTTGA TGACCCAAAC TCCACTCTCT CTGCCTGTCA ATATTGGAGA TCAAGCCTCT	60
ATCTCTTGCA AGTCTACTAA GAGCCTTCTG AATAGTGATG GATTCACTTA TTTGGGCTGG	120
TGCCTGCAGA AGCCAGGCCA GTCTCCACAG CTCCTAATAT ATTTGGTTTC TAATCGATTT	180
TCTGGAGTTC CAGACAGGTT CAGTGGTAGT GGGTCAGGGA CAGATTTTAC CCTCAAGATC	240
AGCAGAGTGG AGGCTGAGGA TTTGGGAGTT TATTATTGCT TCCAGAGTAA CTATCTTCCT	300
CTTACGTTTC GATCGGGGAC CAAGCTGGAA ATAAACGG	339

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Lys Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser	1 5 10 15
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser Trp	20 25 30
Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile Gly	35 40 45
Arg Ile Tyr Pro Val Asn Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys	50 55 60
Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Thr Ala Tyr Met	65 70 75 80
Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala	

[illegible]

Val Tyr Tyr Tyr Asp Gly Ser Ser Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTGCAGCTGC AGGAGTCTGG ACCTGGCCTC GTGAAACCTT CTCAGTCTCT GTCTCTCACC	60
TGCTCTGTCA CTGGCTACTC CATCACCAGT GGTATTACT GGAAGTGGAT CCGGCAGTTT	120
CCAGGAAACA AACTGGAATG GATGGGCTAC ATAAGCTACG ATGGTAGCAA TAACTACAAC	180
CCATCTCTCA AAAATCGAAT CTCCATCACT CGTGACACAT CTAAGAACCA GTTTTTCTCTG	240
AAGTTGAATT CTGTGACTAC TGAGGACACA GCCACATATT ACTGTGCCGT TTATTACTAC	300
GATGGTAGCT CTTTGTACTA CTGGGGCCAA GGGACCACGG TCACCGTCTC CTCA	354

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Arg	1 5 10 15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Gly Val Asp Ser Tyr	20 25 30
Gly Ile Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro	35 40 45
Lys Leu Leu Ile Tyr Arg Ala Ser Tyr Leu Lys Ser Gly Val Pro Ala	50 55 60
Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asp	65 70 75 80
Pro Val Glu Ala Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn	85 90 95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg	

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

GACATTGTGC TGACCCAATC TCCAGCTTCT TTGGCTGTGT CTCTAAGGCA GAGGGCCACC      60
ATATCCTGCA GAGCCAGTGA AGGTGTTGAT AGTTATGGCA TTAGTTTTAT GCACTGGTAC      120
CAGCAGAAAC CAGGACAGCC ACCCAAATC CTCATCTATC GTGCATCCTA CCTAAAATCT      180
GGGTCCCTG CCAGGTTTCTG TGGTAGTGGG TCTAGGACAG ACTTCACCCT CACCATTGAT      240
CCTGTGGAGG CTGATGATGC TGCAACCTAT TACTGTCAGC AAAATAATGA GGATCCGTGG      300
ACGTTCCGGT GAGGCACCAA GCTGGAAATC AAACGG                                336
  
```

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Val Gln Leu Gln Glu Ser Gly Ala Glu Pro Ala Lys Pro Gly Ala Ser
1          5          10          15
Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr Trp
20        25        30
Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
35        40        45
Tyr Ile Asn Pro Ser Ser Gly Tyr Thr Glu Tyr Asn Gln Lys Phe Lys
50        55        60
Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met
65        70        75        80
Gln Leu Ile Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
85        90        95
Arg Arg Gly Asn Tyr Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100       105       110
Val Thr Val Ser Ser
  
```


(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

GTGCAGCTGC AGGAGTCTGG GGCTGAACCG GCAAAACCTG GGGCCTCAGT GAAGATGTCC      60
TGCAAGGCTT CTGGCTACAC CTTTACTACC TACTGGATGC ACTGGGTAAA ACAGAGGCCT      120
GGACAGGGTC TGAATGGAT TGGATACATT AATCCTAGCA GTGGTTATAC TGAGTACAAT      180
CAGAAGTTCA AGGACAAGGC CACATTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG      240
CAACTAATCA GCCTGACATC TGAGGACTCT GCAGTCTATT ACTGTGCAAG AAGGGGTAAT      300
TACTACTACT TTGACTACTG GGGCCAAGGG ACCACGGTCA CCGTCTCCTC A              351

```

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Asp Val Leu Met Thr Gln Thr Pro Lys Phe Leu Pro Val Ser Ala Gly
1           5           10           15
Asp Arg Val Thr Met Thr Cys Lys Ala Ser Gln Ser Val Gly Asn Asn
20        25        30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35        40        45
Tyr Tyr Thr Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50        55        60
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Val
65        70        75        80
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln His Tyr Ser Ser Pro Tyr
85        90        95
Thr Phe Gly Ser Gly Thr Lys Leu Glu
100       105

```

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATGTTTGA TGACCCAAAC TCCAAAATTC CTGCCTGTAT CAGCAGGAGA CAGGGTTACC	60
ATGACCTGCA AGGCCAGTCA GAGTGTGGGT AATAATGTGG CCTGGTACCA ACAGAAGCCA	120
GGACAGTCTC CTAAACTGCT GATATACTAT ACATCCAATC GCTACACTGG AGTCCCTGAT	180
CGCTTCACTG GCAGTGGATC TGGGACAGAT TTCACCTTCA CCATCAGCAG TGTGCAGGTT	240
GAAGACCTGG CAGTTTATTT CTGTCAGCAG CATTATAGCT CTCCGTATAC GTTCGGATCG	300
GGGACCAAGC TGGAG	315

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala	1	5	10	15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser	20	25	30	
Trp Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile	35	40	45	
Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Asp Asn Gly Lys Phe	50	55	60	
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr	65	70	75	80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys	85	90	95	
Ala Arg Ser Tyr Tyr Tyr Asp Gly Ser Pro Trp Phe Thr Tyr Trp Gly	100	105	110	
Gln Gly Thr Leu Val Thr Val Ser Ala	115	120		

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

CAGGTTTCAGC TGCAGCAGTC TGGACCTGAG CTGGTGAAGC CTGGGGCCTC AGTGAAGATT      60
TCCTGCAAGG CTTCTGGCTA TGCATTCAGT AGCTCCTGGA TGAAGTGGGT GAAGCAGAGG      120
CCTGGAAAGG GTCTTGAGTG GATTCGAATT TATCCTGGAG ATGGAGATAC TAACGACAAC      180
GGGAAGTTCA AGGGAGGCAA GGCCACACTG ACCGCAGACA AATCCTCCAG CACAGCCTAC      240
ATGCAACTCA GCAGTCTGAC ATCTGAGGAC TCTGCGGTCT ACTTCTGTGC AAGATCGTAT      300
TACTACGATG GTAGCCCCTG GTTTACTTAC TGGGGCCAAG GGACTCTGGT CACTGTCTCT      360
GCA                                                                    363

```

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1           5           10           15
Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20          25          30
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35          40          45
Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50          55          60
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro
65          70          75          80
Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Ser Glu Phe Pro Trp
85          90          95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100         105

```

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid

(ii) MOLECULE TYPE: cDNA to mRNA

GATATCCAGA	TGACACAGAC	TACATCCTCC	CTGTCTGCCT	CTCTGGGAGA	CAGAGTCACC	60
ATCAGTTGCA	GGGCAAGTCA	GGATATTAGC	AATTATTAA	ACTGGTATCA	GCAGAAACCA	120
GATGGAAGCTG	TTAAACTCCT	GATCTACTAC	ACATCAAGAT	TACACTCAGG	AGTCCCATCA	180
AGGTTCAAGT	GCAGTGGGTC	TGGGACAGAT	TATTCTCTCA	CCATCAGCAA	CCTGGAACCT	240
GAAGATATTG	CCACTTACTT	TTGTCAGCAA	TATAGTGAAT	TTCCGTGGAC	GTTCGGTGGA	300
GGCACCAAGC	TGGAAATCAA	ACGG				324

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

[illegible]

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(ii) MOLECULE TYPE: cDNA to mRNA

CAGGTCCACC	TGCAGCAGTC	TGGAGCTGAG	CTGGTAAGGC	CTGGGACTTC	AGTGAAGATG	60
TCCTGCAAGG	CTGCTGGATA	CACCTTCACT	AACTACTGGA	TAGGTTGGGT	AAAGCAGAGG	120
CCTGGACATG	GCCTTGAGTG	GATTGGATAT	CTTTACCCTG	GAGGTCTTTA	TACTAACTAC	180
AATGAGAAGT	TCAAGGGCAA	GGCCACACTG	ACTGCAGACA	CATCCTCCAG	CACAGCCTAC	240
ATGCAGCTCA	GCAGCCTGAC	ATCTGAGGAC	TCTGCCATCT	ATTACTGTGC	AAGATACAGG	300
GATTACGACT	ATGCTATGGA	CTACTGGGGT	CAAGGAACCT	CAGTCACCGT	CTCCTCA	357

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

[illegible]

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
GATGTTGTTC TGACCCAAAC TCCACTCTCT CTGCCTGTCA ATATTGGAGA TCAAGCCTCT      60
ATCTCTTGCA AGTCTACTAA GAGCCTTCTG AATAGTGATG GATTCACCTA TTTGGGCTGG      120
TGCCTGCAGA AGCCAGGCCA GTCTCCACAG CTCCTAATAT ATTTGGTTTC TAATCGATTT      180
TCTGGAGTTC CAGACAGGTT CAGTGGTAGT GGGTCAGGGA CAGATTTTAC CCTCAAGATC      240
AGCAGAGTGG AGGCTGAGGA TTTGGGAGTT TATTATTGCT TCCAGAGTAA CTATCTTCCT      300
CTTACGTTTCG GATCGGGGAC CAAGCTGGAA ATAAAACGG                                339
```

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1          5          10          15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser
20        25        30
Trp Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile
35        40        45
Gly Arg Ile Tyr Pro Val Asn Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50        55        60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65        70        75        80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85        90        95
Ala Thr Asp Gly Tyr Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr
100       105       110
Val Thr Val Ser Ser
115
```

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

CAGGTTTCAGC	TGCAGCAGTC	TGGACCTGAG	CTGGTGAAGC	CTGGGGCCTC	AGTGAAGATT	60
TCCTGCAAGG	CTTCTGGCTA	TGCATTCACT	AGCTCCTGGA	TGAACTGGGT	GAAACAGAGG	120
CCTGGGAAGG	GTCTTGAGTG	GATTGGACGG	ATTTATCCTG	TAAATGGAGA	TACTAACTAC	180
AATGGGAAGT	TCAAGGGCAA	GGCCACACTG	ACTGCAGACA	AATCCTCCAG	CACAGCCTAC	240
ATGCAACTCA	GCAGCCTGAC	ATCTGAGGAC	TCTGCGGTCT	ACTTCTGTGC	AACCGATGGT	300
TACTGGTACT	TCGATGTCTG	GGGCGCAGGG	ACCACGGTCA	CCGTCTCCTC	A	351

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Asn	Ile	Val	Met	Thr	Gln	Ser	Pro	Lys	Ser	Met	Ser	Met	Ser	Val	Gly
1				5					10					15	
Glu	Arg	Val	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Glu	Asn	Val	Asp	Ile	Tyr
			20					25					30		
Val	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Glu	Gln	Ser	Pro	Lys	Leu	Leu	Ile
		35					40					45			
Tyr	Gly	Thr	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly
	50					55					60				
Ser	Gly	Ser	Ala	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Asn	Val	Gln	Ala
65					70					75				80	
Glu	Asp	Leu	Ser	Asp	Tyr	Tyr	Cys	Val	Gln	Ser	Tyr	Ser	Tyr	Pro	Trp
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg				
			100					105							

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AACATTGTAA TGACCCAATC TCCCAAATCC ATGTCCATGT CAGTAGGAGA GAGGGTCACC	60
TTGAGCTGCA AGGCCAGTGA GAATGTGGAT ATTTATGTAT CCTGGTATCA ACAGAAACCA	120
GAGCAGTCTC CTAAACTGCT GATATACGGG ACATCCAACC GGTACACTGG GGTCCCCGAT	180
CGCTTCACAG GCAGTGGATC TGCAACAGAT TTCACTCTGA CCATCAGCAA TGTGCAGGCT	240
GAAGACCTTT CAGATTATTA CTGTGTACAG AGTTACAGCT ATCCGTGGAC ATTCGGTGGA	300
GGCACCAAGC TGGAAATCAA ACGG	324

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Leu	Ser	His	Lys	Val	Tyr	Met	Arg	Asn	Ser	Lys	Tyr	Pro	Gln
1				5					10				